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SEQUENCE LISTING

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<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009041US

<140> US 09/588,672

<141> 2000-10-10

<150> US 60/158,338

<151> 1999-10-07

<150> US 60/158,425

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<170> PatentIn Ver. 2.1

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<213> Mycobacterium tuberculosis

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<223> Mtb81

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 Val Arg Trp Val Asp Gln Gly Val Gly Cys Ser Lys Val Pro Asp Ile
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 Ala Gly Asp Val Ala Tyr Arg Pro Met Ala Pro Asn Phe Asp Asp Ser
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 gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgtc gggccatcgg 1320
 gctgctttgc ggagcatgct gggccgtgcc ggtgaagtcg gccgcgctgg cccggccatc 1380
 cgtgctgggtg gtgggatagg tgcgggtgat ccgctgcttg cgctggtctt ggtgctggtg 1440
 gtgctgggtca tcgaggcgat ggggtgcgat aggctcaacg ggttgcatct cttcaccgcc 1500
 accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccata 1560
 cggtcggcgc ctactacggg gcgttgccgc tgatcgtcgg gacgctggcg acctcgga 1620

tcgccctgat catcgcggtg ccggtctctg taggagcggc gctggtgatc gtggaacggc 1680
 tgccgaaacg gttggccgag gctgtgggaa tagtcctgga attgctcgcc ggaatcccca 1740
 gcgtggtcgt cggtttgttg ggggcaatga cgttcgggcc gttcatcgct catcacatcg 1800
 ctccggtgat cgctcacaac gtcctccgatg tgccggtgct gaactacttg cgcggcgacc 1860
 cgggcaacgg ggagggcatg ttggtgtccg gtctggtgtt ggcggtgatg gtcgttccca 1920
 ttatcgccac caccactcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
 cgatcgggaa ttc 1993

<210> 8

<211> 374

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> 38kD

<400> 8

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

<210> 9
 <211> 327
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb11 (Tb38-1)

<400> 9
 cggcacgaga gaccgatgcc gctaccctcg cgcaggaggc aggtaatttc gagcggatct 60
 ccggcgacct gaaaacccag atcgaccagg tggagtcgac ggcagggttc ttgcagggcc 120
 agtggcgcg ggcggcgggg acggccgccc aggcgcggt ggtgcgcttc caagaagcag 180
 ccaataagca gaagcaggaa ctgcacgaga tctgcacgaa tattcgtcag gccggcgctcc 240
 aatactcgag ggccgacgag gagcagcagc aggcgctgtc ctgcgaaatg ggcttctgac 300
 ccgctaatac gaaaagaaac ggagcaa 327

<210> 10
 <211> 95
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb11 (Tb38-1)

<400> 10
 Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

<210> 11
 <211> 702
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> TbH4

<220>
 <221> modified_base
 <222> (1)..(702)
 <223> n = g, a, c or t

<400> 11
 cggcagcagg atcggtaccc cgcggcacgc gcagctgccg attcgccggg tttccccacc 60
 cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
 atgaacgggc ggcatacaat tagtgcagga acctttcagt ttagcgacga taatggctat 180
 agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacgggtg gatcagcaag 240
 agattttgaa cagggccaac gaggtggagg ccccgatggc ggaccaccg actgatgtcc 300
 ccatcacacc gtgcgaactc acggnngnta aaaacgccgc ccaacagntg gtnttgtccg 360
 ccgacaacat gcgggaatac ctggcgccgc gtgccaaaga gcggcagcgt ctggcgacct 420
 cgctgcgcaa cgcgcccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
 acaacgacgg cgaaggaact gtgcaggcag aatcggccgg ggccgtcgga ggggacagtt 540
 cggccgaact aaccgatacg ccgaggggtg ccacggccgg tgaacccaac ttcattggatc 600
 tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcacgcgtc gcgcactgng 660
 gggatgggtg gaacacttnc accctgacgc tgcaaggcga cg 702

<210> 12
 <211> 286
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> TbH4

<220>
 <221> MOD_RES
 <222> (1)..(286)
 <223> Xaa = any amino acid

<400> 12
 Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

<210> 13
 <211> 1200
 <212> DNA
 <213> Mycobacterium tuberculosis

<400> 13
 caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
 accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
 tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180

ccgcggaacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
 acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgaccc 300
 gcgacatcct ggagggcgcc aagaaaaggc tcgagttcgt gcgcccgggtg gctgtggacc 360
 tgacctacat cccggtcgtc gggcacgccc tatcgggcgc cttccaggcg ccgttttgcg 420
 cgggcgcgat ggccgtagtg ggcggcgcg cttgcctactt ggtcgtgaaa acgctgatca 480
 acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
 cggacatcat ttccggtatg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
 tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg ggggtgggtga 660
 ccggactggt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
 tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcgggtgcg gccgggtctgt 780
 ccgcacgctc gggcttggct cagcgggata gcctggcgag ctcagccagc ttgcccgccc 840
 tggccggcat tgggggcggg tccgggttttg ggggcttgcc gagcctggct cagggtccatg 900
 ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
 agcaggtcgg cgggcagtcg cagctggctt ccgcgcaggg ttcccaagggt atgggcggac 1020
 ccgtaggcat gggcggcatg caccctctt cgggggcgctc gaaagggacg acgacgaaga 1080
 agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
 acgcgggcgg tgggcaaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

<210> 14

<211> 392

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> HTCC#1 (Mtb40)

<400> 14

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180 185 190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210 215 220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305 310 315 320
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380
Lys Val Leu Val Arg Asn Val Val
385 390

<210> 15
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (1-232)

<220>
<221> CDS
<222> (1)..(720)

<400> 15
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata	96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile	
20 25 30	
ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa	144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys	
35 40 45	
gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt	192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly	
50 55 60	
tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt	240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe	
65 70 75 80	
ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac	288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His	
85 90 95	
gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc	336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala	
100 105 110	
aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac	384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr	
115 120 125	
atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt	432
Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe	
130 135 140	
tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc	480
Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val	
145 150 155 160	
gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa	528
Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Lys Leu Leu Ala Lys	
165 170 175	
ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg	576
Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val	
180 185 190	
gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca	624
Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr	
195 200 205	
aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg	672
Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp	
210 215 220	
gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc taa	720
Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe	
225 230 235 240	
gaattc	726

<210> 16
 <211> 239
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:HTCC#1 (1-232)

 <400> 16
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
 1 5 10 15
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
 130 135 140
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
 145 150 155 160
 Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
 165 170 175
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
 180 185 190
 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
 195 200 205
 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
 210 215 220
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
 225 230 235

 <210> 17
 <211> 661
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:HTCC#1
 (184-392)

<220>
 <221> CDS
 <222> (1)..(651)

 <400> 17
 atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc atc 48
 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
 1 5 10 15

 ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa 96
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 20 25 30

 gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga 144
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 35 40 45

 ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc 192
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60

 ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80

 ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc 288
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 85 90 95

 tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt 336
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 100 105 110

 ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag 384
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 115 120 125

 gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag 432
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 130 135 140

 gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg 480
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 145 150 155 160

 ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg 528
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 165 170 175

 aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act 576
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 180 185 190

 gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 624
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 195 200 205

 aag gtg ctg gta cga aac gtc gtc taa cggcgaattc 661
 Lys Val Leu Val Arg Asn Val Val
 210 215

<210> 18
 <211> 216
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:HTCC#1
 (184-392)

<400> 18
 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
 1 5 10 15
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 20 25 30
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 35 40 45
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 85 90 95
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 100 105 110
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 115 120 125
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 130 135 140
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 145 150 155 160
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 165 170 175
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 180 185 190
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 195 200 205
 Lys Val Leu Val Arg Asn Val Val
 210 215

<210> 19
 <211> 411
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

<220>
 <221> CDS
 <222> (1)..(411)

<400> 19

atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca	48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro	
1 5 10 15	
acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata	96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile	
20 25 30	
ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa	144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys	
35 40 45	
gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt	192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly	
50 55 60	
tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt	240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe	
65 70 75 80	
ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac	288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His	
85 90 95	
gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc	336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala	
100 105 110	
aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac	384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr	
115 120 125	
atc ccg gtc gtc ggg cac gcc cta tag	411
Ile Pro Val Val Gly His Ala Leu	
130 135	

<210> 20
 <211> 136
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

<400> 20

Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro	
1 5 10 15	
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile	
20 25 30	
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys	
35 40 45	
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly	
50 55 60	

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65 70 75 80
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
85 90 95
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
100 105 110
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
115 120 125
Ile Pro Val Val Gly His Ala Leu
130 135

<210> 21
<211> 1225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (TM-1)

<220>
<221> CDS
<222> (4) .. (1215)

<400> 21
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
1 5 10 15
cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
20 25 30
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
35 40 45
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta 192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
50 55 60
ggg tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat 240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
65 70 75
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc 288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
80 85 90 95
cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc 336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly
100 105 110
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc 384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
115 120 125

tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg 432
 Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro
 130 135 140

ttt tgc gcg ggc gcg atg gcc gta gtg ggc gcc gcg ctt aag ctt gcc 480
 Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala
 145 150 155

tac ttg gtc gtg aaa acg ctg atc aac gcg aag ctt act caa ctc ctc 528
 Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu
 160 165 170 175

aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac 576
 Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp
 180 185 190

atc att tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg 624
 Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val
 195 200 205

tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac 672
 Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp
 210 215 220

aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac 720
 Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn
 225 230 235

ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc 768
 Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser
 240 245 250 255

ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca 816
 Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala
 260 265 270

tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg 864
 Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
 275 280 285

ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg 912
 Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro
 290 295 300

agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc 960
 Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro
 305 310 315

cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc gcc ggg cag 1008
 Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln
 320 325 330 335

tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta 1056
 Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
 340 345 350

ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg 1104
 Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
 355 360 365

acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag 1152
 Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
 370 375 380

cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta 1200
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
 385 390 395

cga aac gtc gtc taa cggcgaattc 1225
 Arg Asn Val Val
 400

<210> 22
 <211> 403
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:HTCC#1 (TM-1)

<400> 22
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
 1 5 10 15
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
 130 135 140
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala Tyr
 145 150 155 160
 Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu Lys
 165 170 175
 Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile
 180 185 190
 Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp
 195 200 205
 Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
 210 215 220

Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
 225 230 235 240
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
 245 250 255
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
 260 265 270
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
 275 280 285
 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
 290 295 300
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
 305 310 315 320
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
 325 330 335
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
 340 345 350
 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
 355 360 365
 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
 370 375 380
 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
 385 390 395 400
 Asn Val Val

<210> 23
 <211> 1225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (TM-2)

<220>
 <221> CDS
 <222> (4)..(1215)

<400> 23
 cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
 1 5 10 15
 cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
 Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
 20 25 30
 ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144
 Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
 35 40 45

aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta	192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu	
50 55 60	
ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat	240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn	
65 70 75	
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc	288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile	
80 85 90 95	
cac gac cag gcc aac gcg gtc cag acg acc cgc gac aag ctt atc ctg	336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu	
100 105 110	
gag ggc gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac	384
Glu Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp	
115 120 125	
ctg acc tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag	432
Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln	
130 135 140	
gcg ccg ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc	480
Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala	
145 150 155	
tac ttg gtc gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg	528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu	
160 165 170 175	
ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att	576
Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile	
180 185 190	
tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag	624
Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu	
195 200 205	
ttc atc aca aac gcg aag ctt ctc aac ggc ctg aaa gag ctt tgg gac	672
Phe Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp	
210 215 220	
aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac	720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn	
225 230 235	
ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc	768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser	
240 245 250 255	
ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca	816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala	
260 265 270	
tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg	864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu	
275 280 285	

ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg 912
 Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro
 290 295 300

agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc 960
 Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro
 305 310 315

cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag 1008
 Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln
 320 325 330 335

tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta 1056
 Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
 340 345 350

ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg 1104
 Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
 355 360 365

acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag 1152
 Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
 370 375 380

cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta 1200
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
 385 390 395

cga aac gtc gtc taa cggcgaattc 1225
 Arg Asn Val Val
 400

<210> 24
 <211> 403
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:HTCC#1 (TM-2)

<400> 24
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
 1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu Glu
 100 105 110

Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu
 115 120 125
 Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala
 130 135 140
 Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr
 145 150 155 160
 Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu
 165 170 175
 Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser
 180 185 190
 Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe
 195 200 205
 Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
 210 215 220
 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
 225 230 235 240
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
 245 250 255
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
 260 265 270
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
 275 280 285
 Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
 290 295 300
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
 305 310 315 320
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
 325 330 335
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
 340 345 350
 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
 355 360 365
 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
 370 375 380
 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
 385 390 395 400
 Asn Val Val

<210> 25
 <211> 3058
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>

<223> TbH9 (Mt b39A)

<400> 25

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gatcgtaccc gtgcgagtgc tcgggcccgtt tgaggatgga gtgcacgtgt ctttcgtgat 60
ggcataccca gagatgttgg cggcggcgcc tgacaccctg cagagcatcg gtgctaccac 120
tgtggctagc aatgccgctg cggcggcccc gacgactggg gtgggtgccc ccgctgccga 180
tgagggtgctg gcgctgactg cggcgcactt cgccgcacat gcggcgatgt atcagtccgt 240
gagcgcctcgg gctgctgcga ttcattgacca gttcgtggcc acccttgcca gcagcgccag 300
ctcgtatgcg gccactgaag tcgccaatgc ggcggcgggc agctaagcca ggaacagtcg 360
gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
agatcaactc cgcgaggatg tacgccggcc cgggttcggc ctgctggtg gcccgggctc 480
agatgtggga cagcgtggcg agtgacctgt tttcggccgc gtcggcggtt cagtcgggtg 540
tctggggctc gagcgtgggg tcgtggatag gttcgtcggc ggggtctgat gtggcgggcg 600
cctcgccgta tgtggcgtgg atgagcgtca ccgcggggca ggccgagctg accgcggccc 660
aggtccgggt tgcctgcggc gcctacgaga cggcgatagg gctgacggtg ccccgccgg 720
tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
acacccgggc gatcgcggtc aacgaggccg aatacggcga gatgtggggc caagacggcg 840
ccgcgatggt tggctacgcc gcggcgacgg cgacggcgac ggcgacgttg ctgccgttcg 900
aggaggcgcc ggagatgacc agcgcgggtg ggctcctcga gcaggccggc gcggtcgagg 960
aggcctccga caccgcggcg gcgaaccagt tgatgaacaa tctgccccag gcgctgcaac 1020
agctggccca gccacgcag ggcaccacgc cttcttccaa gctgggtggc ctgtggaaga 1080
cggctctgcc gcatcggtcg ccgatcagca acatggtgtc gatggccaac aaccacatgt 1140
cgatgaccaa ctccgggtgtg tcgatgacca acacctgag ctcatgttg aagggtttt 1200
ctccggcgcc ggccgcccag gccgtgcaaa ccgcggcgca aaacggggtc cggcgcatga 1260
gctcgctggg cagctcgctg ggttcttcgg gtctggcgcg tggggtggcc gccaaacttg 1320
gtcgggcggc ctccggtcgg tcgttgctcg tgccgcaggc ctgggcccgc gccaaaccag 1380
cagtcacccc ggccggcgcg gcgctgcgc tgaccagcct gaccagcgcc gcggaagag 1440
ggcccgggca gatgctggg gccgtgcgg tggggcagat gggcgccagg gccggtggtg 1500
ggctcagtg tgtgctgcgt gttccgcgc gacctatgt gatgccgat tctccggcg 1560
ccggttagga gaggggcgcg agactgtcgt tatttgacca gtgacggcg gtctcgggtg 1620
ttccgcggcc ggctatgaca acagtcaatg tgcattgaca gttacaggta ttaggtccag 1680
gttcaacaag gagacaggca acatggcctc acgttttatg acggatccgc acgcgatgcg 1740
ggacatggcg gccggttttg aggtgcacgc ccagacggtg gaggacgagg ctccgcccgt 1800
gtgggcgtcc gcgcaaaaca tttccggtgc gggctggagt ggcattggcg aggcgacctc 1860
gctagacacc atggcccaga tgaatcaggc gtttcgcaac atcgtgaaca tgctgacgg 1920
ggtgcgtgac gggctgggtc gcgacgcca caactacgag cagcaagagc aggcctccca 1980
gcagatcctc agcagctaac gtcagccgt gcagcacaat acttttaca gcgaaggaga 2040
acaggttcga tgaccatcaa ctatcaattc ggggatgtcg acgctcacgg cgccatgatc 2100
cgcgctcagg ccgggttgct ggaggccgag catcaggcca tcattcgtga tgtgttgacc 2160
gcgagtgaat tttggggcg cgccggttcg gcggcctgcc aggggttcat taccagttg 2220
ggccgtaact tccaggtgat ctacgagcag gccaacgcc acgggcagaa ggtgcaggct 2280
gccggcaaca acatggcgca aaccgacag gccgtcggct ccagctgggc ctgacaccag 2340
gccaaggcca gggacgtggt gtacgagtga agttcctcgc gtgaccttc ggggtggcag 2400
ctaagtggtc agtgctgggg tgttggtggt ttgctgcttg gcggttctt cgggtgctgg 2460
cagtgctgct cgggctcggg tgaggacctc gaggccaggg tagcgccgtc cttcgatcca 2520
ttcgtcgtgt tgttcggcga ggacggctcc gacgaggcgg atgacgagg cgcggtcggg 2580
gaagatgccc acgacgtcgg ttcggcgctg tacctctcgg ttgaggcgtt cctgggggtt 2640
gttgaccag atttggcgcc agatctgctt ggggaaggcg gtgaacgcca gcaggtcgg 2700
gcgggcggtg tcgaggtgct cgccaccgc ggggagtttg tcggtcagag cgtcgagtac 2760
ccgatcatat tgggcaacaa ctgattcggc gtcgggctgg tcgtagatgg agtgcagcag 2820
ggtgcgcacc cagggccagg agggcttcgg ggtggctgcc atcagattgg ctgcgtagtg 2880
ggttctgcag cgctgccagg ccgctgcgg cagggtggcg ccgatcgcg ccaccaggcc 2940
ggcgtggggc tcgctggtga ccagcgcgac ccggacagg ccgcggcgca ccaggtcgg 3000
gaagaacgcc agccagccgg ccccgctctc ggcggaggtg acctggatgc ccaggatc 3058
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<210> 26

<211> 391

<212> PRT

<213> Mycobacterium tuberculosis

<220>
 <223> TbH9 (Mtb39A)

 <400> 26
 Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160
 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

<210> 27
 <211> 447
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa12

<400> 27
 cggatatgaac acggccgcgt ccgataactt ccagctgtcc caggggtgggc agggattcgc 60
 cattccgatac gggcaggcga tggcgatcgc gggccagatc cgatcgggtg ggggggtcacc 120
 caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
 cggcgcacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaacc cgatggcgga 300
 cgcgcttaac gggcatcatc ccggtgacgt catctcgggtg aactggcaaa ccaagtcggg 360
 cggcacgcgt acagggaacg tgacattggc cgaggggaccc ccggcctgat ttcgtcgygg 420
 ataccacccg ccggccggcc aattgga 447

<210> 28
 <211> 132
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa12

<400> 28
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125
Gly Pro Pro Ala
130

<210> 29
<211> 1872
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbRa35 (Mtb32A)

<400> 29
gactacgttg gtgtagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60
tagctacccc gacacaggag gttacgggat gagcaattcg cgccgccgct cactcagggtg 120
gtcatgggtg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
ggcggccccg ccggccttgt cgcaggaccg gttcgccgac ttccccgcgc tgccccctga 240
cccgtccgcg atggctgccc aagtggcgcc acagggtggc aacatcaaca ccaaactggg 300
ctacaacaac gccgtgggag ccgggaccgg catcgatcat gatcccaacg gtgtcgtgct 360
gaccaacaac cacgtgatcg cgggcgccac cgacatcaat gcgttcagcg tgggtcccg 420
ccaaacctac ggcgtcgatg tggctgggta tgaccgcacc caggatgtcg cgggtcgtga 480
gctgcgcggt gccggtggcc tgccgtcgcc ggcatcggt ggccggcgctg cgggttgggtga 540
gcccgtcgtc gcgatgggca acagcgggtg gcagggcgga acgccccgtg cgggtgcctgg 600
caggggtggtc gcgctcgccc aaaccgtgca ggcgtcggt tgcgtgaccg gtgccgaaga 660
gacattgaac ggggtgatcc agttcgatgc cgcaatccag cccggtgatt cgggcggggc 720
cgctcgtaac ggcctaggac aggtgggtcg tatgaacacg gccgcgtccg ataacttcca 780
gctgtcccag ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgcggg 840
ccaaatccga tcgggtgggg ggtcaccac cggttcatac gggcctaccg ccttcctcgg 900
cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
tccggcgcca agtctcggca tctccaccgg cgacgtgat accgcggtcg acggcgctcc 1020
gatcaactcg gccaccgcga tggcggaacg gcttaacggg catcatcccg gtgacgtcat 1080
ctcgggtgaac tggcaaacca agtcggggcg cacgcgtaca gggaacgtga cattggccga 1140
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cagccgtgat tgccgcgtga gccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
gcaatgaacg aggcagaaca cagcgttgag caccctcccg tgcagggcag ttacgtcgaa 1320
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gatccgacct ggtttaagca cgcgctcttc tacgaggtgc tggtcggggc gttcttcgac 1440
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tggtttggca tcgactgcat ctgttgccgc cgttcctacg actcaccgct gcgcgacggc 1560
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aatcacacct cggagtgcga cccctggttt caggagtcgc gccgcgaccc agacggaccg 1740
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ttcgtcgaca ccgaagagtc gaactgggtc ttgatcctg tccgccgaca gtttctactg 1860
gcaccgattc tt 1872

<210> 30
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

<220>
 <223> TbRa35 (Mtb32A)
 <400> 30
 Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320

Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350

Pro Pro Ala
 355

<210> 31
 <211> 1441
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTCC#2 (Mtb41)

<400> 31

gaggttgctg	gcaatggatt	tcggtgtttt	acctccggaa	gtgaattcaa	gccgaatgta	60
ttccggtccg	gggcccggagt	cgatgctagc	cgccgcggcc	gcctgggacg	gtgtggccgc	120
ggagttgact	tccgccgcgg	tctcgtatgg	atcgggtggtg	tcgacgctga	tcgttgagcc	180
gtggatgggg	ccggcggcgg	ccgcgatggc	ggccgcggca	acgccgtatg	tgggggtggct	240
ggccgccacg	gcggcgctgg	cgaaggagac	ggccacacag	gcgagggcag	cggcggaagc	300
gtttgggacg	gcgttcgcga	tgacgggtgcc	accatccctc	gtcgcggcca	accgcagccg	360
gttgatgtcg	ctgggtcgcg	cgaacattct	ggggcaaaac	agtgcggcga	tcgcggctac	420
ccaggccgag	tatgccgaaa	tgtgggcca	agacgctgcc	gtgatgtaca	gctatgaggg	480
ggcatctcg	gccgcgtcgg	cgttgccgcc	gttcactcca	cccgtagaag	gcaccggccc	540
ggccggggccc	gcggccgcag	ccgcggcgac	ccaagccgcc	ggtgcggggc	ccgttgcgga	600
tgcacaggcg	acactggccc	agctgcccc	ggggatcctg	agcgacattc	tgtccgcatt	660
ggccgccaac	gctgatccgc	tgacatcggg	actgttgggg	atcgcgtcga	ccctcaaccc	720
gcaagtcgga	tccgctcagc	cgatagtgat	ccccacccc	ataggggaat	tggacgtgat	780
cgcgctctac	attgcatcca	tcgcgaccgg	cagcatttgc	ctcgcgatca	cgaacacggc	840
cagaccctgg	cacatcgggc	tatacgggaa	cgccggcggg	ctgggaccga	cgcagggcca	900
tccactgagt	tcggcgaccg	acgagccgga	gccgcactgg	ggcccccttc	ggggcgcggc	960
gccggtgtcc	gcgggcgtcg	gccacgcagc	attagtcgga	gcgttgtcgg	tgccgcacag	1020
ctggaccacg	gccgccccgg	agatccagct	cgccgttcag	gcaacaccca	ccttcagctc	1080
cagcgccggc	gccgacccga	cgcccctaaa	cgggatgccg	gcaggcctgc	tcagcgggat	1140
ggctttggcg	agcctggccg	cacgcggcac	gacgggcggg	ggcggcacc	gtagcggcac	1200
cagcactgac	ggccaagagg	acggccgcaa	acccccggta	gttgtgatta	gagagcagcc	1260
gccgcccgga	aacccccgc	ggtaaaagtc	cggcaaccgt	tcgtcgccgc	gcggaaaatg	1320
cctggtgagc	gtggctatcc	gacgggcgt	tcacaccgct	tgtagtagcg	tacggctatg	1380
gacgacgggtg	tctggattct	cggcggctat	cagagcgatt	ttgctcgcaa	cctcagcaaa	1440
g						1441

<210> 32
 <211> 423
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTTC#2 (Mtb41)

<400> 32

Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
1				5					10					15	

Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
 20 25 30
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
 85 90 95
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335

Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

<210> 33
 <211> 1742
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI-A)

<220>
 <221> modified_base
 <222> (1)..(1742)
 <223> n = g, a, c or t

<400> 33
 ccgctctctt tcaacgtcat aagttcgggt ggccagtcgg ccgcgcgtgc atatggcacc 60
 aataacgcgt gtcccatgga taccgcgacc gcacgcaggt agagcggatc agcgcagccg 120
 gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
 ttctcatggt cgttaacgcc ttccaacact gcgacgggtgc gcgccccggc gaccacctga 240
 gcaacgctcg gctccggcac ccggcgcgcg gctgccaaca cccacgatt gagatggaag 300
 ccgatcacc gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
 agatcatcct tgagctcggc cagccggcgg tgggtgccga acagcgccag cggcgtgaac 420
 cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
 gtcggcagat cgggacnaen gtcgatgctg ttcagggtcac ggaaatcgtc gagccgtggg 540
 tcgtcgggat cgcagacgtc ctgaacatcg aggcgcgtcg ggtgctgggc acaacggcct 600
 tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
 cacgctcgtc gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
 tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
 ctggcagctg cggcgccgaa cctacagggt attggcacga caatgaacgc ccagaacgcg 840
 gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgtg 900
 accgcggctc agtttgctgc gcacgcgcag atgtaccaa cggtcagcgc ccaggccgcg 960
 gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
 gaggcgccca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
 ggggaacatc cggagtcttc gggtcagggg ttgcgccagc gccagccga ttcagntatc 1140
 ggcgtccata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
 cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
 cccagacggt ggaggacgag gctcgccgga tgtggcgctc cgcgcaaac atttccgggtg 1320
 cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
 cgtttcgcaa catcgtgaac atgctgcacg ggggtcgtga cgggctgggt cgcgacgcca 1440
 acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgcgaaagc 1500
 cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
 cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgctcg ttgaggcgga 1620
 gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680

ggtaggttgc caggagttca ttaccaggtt gggccgtaac ttccaggtga tctacgagca 1740
gg 1742

<210> 34
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI-A)

<400> 34
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 35
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 35
tggattccga tagcggtttc ggcccctcga cgggcgacca cggcgcgag gcctccgaac 60
ggggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccggggcg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccggtac 300
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggc caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcgggc tttcaggccg 480
cccatgcccg gtttggtggc gcggccgcca aagtcaacac cttgttggtat gtcgcgagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgcca tgctg 585

<210> 36
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 36
 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

<210> 37
 <211> 500
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 37
 cgtggcaatg tcgttgaccg tcggggcccg ggtcgctcc gcagatcccg tggacgcggt 60
 cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
 ggctgccgca cagttcaacg cctcaccggg ggcgcagctc tatttgcgca atttcctcgc 180
 cgcaccgccca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcggc 240
 acagtacatc ggccttgctg agtcgggtgc cggctcctgc aacaactatt aagcccatgc 300
 gggccccatc ccgcgaccgc gcatcgctgc cggggctagg ccagattgcc ccgctcctca 360
 acggggccgca tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
 caacggggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
 gccgccaccg cgggtggagct 500

<210> 38
 <211> 96
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 38
 Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
 1 5 10 15
 Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
 20 25 30
 Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
 35 40 45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
 50 55 60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

<210> 39
 <211> 999
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> DPEP

<400> 39
 atgcatcacc atcaccatca catgcatcag gtggacccca acttgacacg tcgcaaggga 60
 cgattggcgg cactggctat cgcggcgatg gccagcgcca gcctgggtgac cgttgcggtg 120
 cccgcgaccg ccaacgccga tccggagcca gcgccccggg taccacaac ggccgcctcg 180
 ccgccgtcga ccgctgcagc gccaccgcga ccggcgacac ctggtgcccc cccaccaccg 240
 gccgcgcgca acacgccgaa tgcccagccg ggcgatccca acgcagcacc tccgcgggcc 300
 gaccgaacg caccgccgcc acctgtcatt gcccacaacg caccacaacc tgtccggatc 360
 gacaaccggg ttggaggatt cagcttcgag ctgcctgctg gctgggtgga gtctgacgcc 420
 gcccaacttcg actacggttc agcactcctc agcaaaaacca ccggggaccc gccatttccc 480
 ggacagccgc cgccgggtggc caatgacacc cgtatcgtgc tcggccgggt agacaaaag 540
 ctttacgcca gcgcggaagc caccgactcc aaggccgcgg ccggttggtg ctcgacatg 600
 ggtgagttct atatgcccta cccgggcacc ccgatcaacc aggaaccgt ctcgctcgac 660
 gccaacgggg tgtctggaag cgcgtcgtat tacgaagtca agttcagcga tccgagtaag 720
 ccgaacggcc agatctggac gggcgtaatc ggctcgcccg cggcgaaacg accggacgcc 780
 gggccccctc agcgttggtt tgtggtatgg ctcgggaccg ccaacaaccc ggtggacaag 840
 ggcgcgccca aggcgtggc cgaatcgatc cggcctttgg tcgccccgcc gccggcgccg 900
 gcaccggctc ctgcagagcc cgctccggcg ccggcgccgg ccgggggaag cgctcctacc 960
 ccgacgacac cgacaccgca gcggacctta ccggcctga 999

<210> 40
 <211> 332
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> DPEP

<400> 40
 Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115 120 125

Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160

Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175

Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190

Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205

Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220

Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240

Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255

Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270

Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285

Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300

Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320

Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

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<210> 41
<400> 41
000
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<210> 42
<400> 42
000
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<210> 43
<211> 339
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 43
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tttctgcct cggttgccag cgcagatcca cctgacccgc atcagccgga catgacgaaa 120
ggctattgcc cgggtggccg atgggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180
taccgccgacg gctcgttttg gcaccagtgg atgcaaactg gggttaccgg cccacagttt 240
tacttcgatt gtgtcagcgg cggtagagccc ctccccggcc cgccgccacc ggggtggttg 300
ggtaggggcaa ttccgtccga gcagcccaac gtcacctga 339

<210> 44
<211> 112
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 44
Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100 105 110

<210> 45
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 45
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 46
 <211> 51
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

<400> 46
 Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

<210> 47
 <211> 2310
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb82

<400> 47
 ccagcccccg ccccgccac gccgaggtat gtggactgat ggccaaagcg tcagagaccg 60
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 gacccctgag caccagggcg gtgttccgcc cggatttcgg cgatgaggac aacttcccc 180
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<210> 48

<211> 750

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> Mtb82

<400> 48

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 35 40 45
 Pro Thr Leu Gly Pro Asp Thr Glu Pro Gln Asp Arg Met Ala Thr Thr
 50 55 60
 Ser Arg Val Arg Pro Pro Val Arg Arg Leu Gly Gly Gly Leu Val Glu
 65 70 75 80
 Ile Pro Arg Ala Pro Asp Ile Asp Pro Leu Glu Ala Leu Met Thr Asn
 85 90 95
 Pro Val Val Pro Glu Ser Lys Arg Phe Cys Trp Asn Cys Gly Arg Pro
 100 105 110
 Val Gly Arg Ser Asp Ser Glu Thr Lys Gly Ala Ser Glu Gly Trp Cys
 115 120 125
 Pro Tyr Cys Gly Ser Pro Tyr Ser Phe Leu Pro Gln Leu Asn Pro Gly
 130 135 140
 Asp Ile Val Ala Gly Gln Tyr Glu Val Lys Gly Cys Ile Ala His Gly
 145 150 155 160
 Gly Leu Gly Trp Ile Tyr Leu Ala Leu Asp Arg Asn Val Asn Gly Arg
 165 170 175
 Pro Val Val Leu Lys Gly Leu Val His Ser Gly Asp Ala Glu Ala Gln
 180 185 190
 Ala Met Ala Met Ala Glu Arg Gln Phe Leu Ala Glu Val Val His Pro
 195 200 205
 Ser Ile Val Gln Ile Phe Asn Phe Val Glu His Thr Asp Arg His Gly
 210 215 220

Asp Pro Val Gly Tyr Ile Val Met Glu Tyr Val Gly Gly Gln Ser Leu
 225 230 235 240
 Lys Arg Ser Lys Gly Gln Lys Leu Pro Val Ala Glu Ala Ile Ala Tyr
 245 250 255
 Leu Leu Glu Ile Leu Pro Ala Leu Ser Tyr Leu His Ser Ile Gly Leu
 260 265 270
 Val Tyr Asn Asp Leu Lys Pro Glu Asn Ile Met Leu Thr Glu Glu Gln
 275 280 285
 Leu Lys Leu Ile Asp Leu Gly Ala Val Ser Arg Ile Asn Ser Phe Gly
 290 295 300
 Tyr Leu Tyr Gly Thr Pro Gly Phe Gln Ala Pro Glu Ile Val Arg Thr
 305 310 315 320
 Gly Pro Thr Val Ala Thr Asp Ile Tyr Thr Val Gly Arg Thr Leu Ala
 325 330 335
 Ala Leu Thr Leu Asp Leu Pro Thr Arg Asn Gly Arg Tyr Val Asp Gly
 340 345 350
 Leu Pro Glu Asp Asp Pro Val Leu Lys Thr Tyr Asp Ser Tyr Gly Arg
 355 360 365
 Leu Leu Arg Arg Ala Ile Asp Pro Asp Pro Arg Gln Arg Phe Thr Thr
 370 375 380
 Ala Glu Glu Met Ser Ala Gln Leu Thr Gly Val Leu Arg Glu Val Val
 385 390 395 400
 Ala Gln Asp Thr Gly Val Pro Arg Pro Gly Leu Ser Thr Ile Phe Ser
 405 410 415
 Pro Ser Arg Ser Thr Phe Gly Val Asp Leu Leu Val Ala His Thr Asp
 420 425 430
 Val Tyr Leu Asp Gly Gln Val His Ala Glu Lys Leu Thr Ala Asn Glu
 435 440 445
 Ile Val Thr Ala Leu Ser Val Pro Leu Val Asp Pro Thr Asp Val Ala
 450 455 460
 Ala Ser Val Leu Gln Ala Thr Val Leu Ser Gln Pro Val Gln Thr Leu
 465 470 475 480
 Asp Ser Leu Arg Ala Ala Arg His Gly Ala Leu Asp Ala Asp Gly Val
 485 490 495
 Asp Phe Ser Glu Ser Val Glu Leu Pro Leu Met Glu Val Arg Ala Leu
 500 505 510
 Leu Asp Leu Gly Asp Val Ala Lys Ala Thr Arg Lys Leu Asp Asp Leu
 515 520 525
 Ala Glu Arg Val Gly Trp Arg Trp Arg Leu Val Trp Tyr Arg Ala Val
 530 535 540

Ala Glu Leu Leu Thr Gly Asp Tyr Asp Ser Ala Thr Lys His Phe Thr
545 550 555 560

Glu Val Leu Asp Thr Phe Pro Gly Glu Leu Ala Pro Lys Leu Ala Leu
565 570 575

Ala Ala Thr Ala Glu Leu Ala Gly Asn Thr Asp Glu His Lys Phe Tyr
580 585 590

Gln Thr Val Trp Ser Thr Asn Asp Gly Val Ile Ser Ala Ala Phe Gly
595 600 605

Leu Ala Arg Ala Arg Ser Ala Glu Gly Asp Arg Val Gly Ala Val Arg
610 615 620

Thr Leu Asp Glu Val Pro Pro Thr Ser Arg His Phe Thr Thr Ala Arg
625 630 635 640

Leu Thr Ser Ala Val Thr Leu Leu Ser Gly Arg Ser Thr Ser Glu Val
645 650 655

Thr Glu Glu Gln Ile Arg Asp Ala Ala Arg Arg Val Glu Ala Leu Pro
660 665 670

Pro Thr Glu Pro Arg Val Leu Gln Ile Arg Ala Leu Val Leu Gly Gly
675 680 685

Ala Leu Asp Trp Leu Lys Asp Asn Lys Ala Ser Thr Asn His Ile Leu
690 695 700

Gly Phe Pro Phe Thr Ser His Gly Leu Arg Leu Gly Val Glu Ala Ser
705 710 715 720

Leu Arg Ser Leu Ala Arg Val Ala Pro Thr Gln Arg His Arg Tyr Thr
725 730 735

Leu Val Asp Met Ala Asn Lys Val Arg Pro Thr Ser Thr Phe
740 745 750

<210> 49
<211> 1920
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb59

<400> 49
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cgtctgcgtc gacaccatcc tcaaccagcg gcagaactgg gaggccgggtg atccaagaa 660
gcagggtgcgc tgtgtatacg tggccatcgg gcagaaggga actaccatcg ccgcggttacg 720

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gatgtacgag ggcaagcatg tgctgatcat cttcgacgac ctgactaagc aggccgagcg 900
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<210> 50
 <211> 549
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb59

<400> 50
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 35 40 45
 Ser Val Met Thr Gln Glu Leu Leu Glu Phe Pro Gly Gly Ile Leu Gly
 50 55 60
 Val Ala Leu Asn Leu Asp Glu His Ser Val Gly Ala Val Ile Leu Gly
 65 70 75 80
 Asp Phe Glu Asn Ile Glu Glu Gly Gln Gln Val Lys Arg Thr Gly Glu
 85 90 95
 Val Leu Ser Val Pro Val Gly Asp Gly Phe Leu Gly Arg Val Val Asn
 100 105 110
 Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
 115 120 125
 Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val His Arg Gln Gly
 130 135 140
 Val Lys Glu Pro Leu Gln Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175
 Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Arg Gln Asn
 180 185 190
 Trp Glu Ser Gly Asp Pro Lys Lys Gln Val Arg Cys Val Tyr Val Ala
 195 200 205
 Ile Gly Gln Lys Gly Thr Thr Ile Ala Ala Val Arg Arg Thr Leu Glu
 210 215 220
 Glu Gly Gly Ala Met Asp Tyr Thr Thr Ile Val Ala Ala Ala Ala Ser
 225 230 235 240
 Glu Ser Ala Gly Phe Lys Trp Leu Ala Pro Tyr Thr Gly Ser Ala Ile
 245 250 255
 Ala Gln His Trp Met Tyr Glu Gly Lys His Val Leu Ile Ile Phe Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
 290 295 300
 His Ser Arg Leu Leu Glu Arg Cys Ala Lys Leu Ser Asp Asp Leu Gly
 305 310 315 320
 Gly Gly Ser Leu Thr Gly Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Ile Ser Ala Tyr Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Cys Phe Leu Glu Thr Asp Leu Phe Asn Gln Gly Val Arg Pro Ala Ile
 355 360 365
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Ile Lys
 370 375 380
 Ala Met Lys Glu Val Ala Gly Ser Leu Arg Leu Asp Leu Ser Gln Tyr
 385 390 395 400
 Arg Glu Leu Glu Ala Phe Ala Ala Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ala Gln Leu Glu Arg Gly Ala Arg Leu Val Glu Leu Leu Lys
 420 425 430
 Gln Pro Gln Ser Gln Pro Met Pro Val Glu Glu Gln Val Val Ser Ile
 435 440 445
 Phe Leu Gly Thr Gly Gly His Leu Asp Ser Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Thr Glu Leu Leu Asp His Met Arg Ala Ser Glu Glu
 465 470 475 480


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acaaggccgt ggtcgcgctg catgaagcgt tcgggctcgg cggcgacgag gagggccacg 3480
tgtacgcggg gacgggacgg tagatggggc tgtcaatagt gaa 3523

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<210> 52

<211> 1172

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF14 fusion protein

<400> 52

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Pro Gly Thr Asp Ile Asp Pro Asp Ser Phe Trp Ala Gly Val Asp Lys
                35                      40          45
Val Val Ala Asp Leu Thr Pro Gln Asn Gln Ala Leu Leu Asn Ala Arg
                50                      55          60
Asp Glu Leu Gln Ala Gln Ile Asp Lys Trp His Arg Arg Arg Val Ile
        65                      70          75          80
Glu Pro Ile Asp Met Asp Ala Tyr Arg Gln Phe Leu Thr Glu Ile Gly
                85                      90          95
Tyr Leu Leu Pro Glu Pro Asp Asp Phe Thr Ile Thr Thr Ser Gly Val
                100                     105          110
Asp Ala Glu Ile Thr Thr Thr Ala Gly Pro Gln Leu Val Val Pro Val
                115                     120          125

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Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser
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 Leu Tyr Asp Ala Leu Tyr Gly Thr Asp Val Ile Pro Glu Thr Asp Gly
 145 150 155 160
 Ala Glu Lys Gly Pro Thr Tyr Asn Lys Val Arg Gly Asp Lys Val Ile
 165 170 175
 Ala Tyr Ala Arg Lys Phe Leu Asp Asp Ser Val Pro Leu Ser Ser Gly
 180 185 190
 Ser Phe Gly Asp Ala Thr Gly Phe Thr Val Gln Asp Gly Gln Leu Val
 195 200 205
 Val Ala Leu Pro Asp Lys Ser Thr Gly Leu Ala Asn Pro Gly Gln Phe
 210 215 220
 Ala Gly Tyr Thr Gly Ala Ala Glu Ser Pro Thr Ser Val Leu Leu Ile
 225 230 235 240
 Asn His Gly Leu His Ile Glu Ile Leu Ile Asp Pro Glu Ser Gln Val
 245 250 255
 Gly Thr Thr Asp Arg Ala Gly Val Lys Asp Val Ile Leu Glu Ser Ala
 260 265 270
 Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala
 275 280 285
 Ala Asp Lys Val Leu Gly Tyr Arg Asn Trp Leu Gly Leu Asn Lys Gly
 290 295 300
 Asp Leu Ala Ala Ala Val Asp Lys Asp Gly Thr Ala Phe Leu Arg Val
 305 310 315 320
 Leu Asn Arg Asp Arg Asn Tyr Thr Ala Pro Gly Gly Gly Gln Phe Thr
 325 330 335
 Leu Pro Gly Arg Ser Leu Met Phe Val Arg Asn Val Gly His Leu Met
 340 345 350
 Thr Asn Asp Ala Ile Val Asp Thr Asp Gly Ser Glu Val Phe Glu Gly
 355 360 365
 Ile Met Asp Ala Leu Phe Thr Gly Leu Ile Ala Ile His Gly Leu Lys
 370 375 380
 Ala Ser Asp Val Asn Gly Pro Leu Ile Asn Ser Arg Thr Gly Ser Ile
 385 390 395 400
 Tyr Ile Val Lys Pro Lys Met His Gly Pro Ala Glu Val Ala Phe Thr
 405 410 415
 Cys Glu Leu Phe Ser Arg Val Glu Asp Val Leu Gly Leu Pro Gln Asn
 420 425 430
 Thr Met Lys Ile Gly Ile Met Asp Glu Glu Arg Arg Thr Thr Val Asn
 435 440 445

Leu Lys Ala Cys Ile Lys Ala Ala Ala Asp Arg Val Val Phe Ile Asn
 450 455 460
 Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu
 465 470 475 480
 Ala Gly Pro Met Val Arg Lys Gly Thr Met Lys Ser Gln Pro Trp Ile
 485 490 495
 Leu Ala Tyr Glu Asp His Asn Val Asp Ala Gly Leu Ala Ala Gly Phe
 500 505 510
 Ser Gly Arg Ala Gln Val Gly Lys Gly Met Trp Thr Met Thr Glu Leu
 515 520 525
 Met Ala Asp Met Val Glu Thr Lys Ile Ala Gln Pro Arg Ala Gly Ala
 530 535 540
 Ser Thr Ala Trp Val Pro Ser Pro Thr Ala Ala Thr Leu His Ala Leu
 545 550 555 560
 His Tyr His Gln Val Asp Val Ala Ala Val Gln Gln Gly Leu Ala Gly
 565 570 575
 Lys Arg Arg Ala Thr Ile Glu Gln Leu Leu Thr Ile Pro Leu Ala Lys
 580 585 590
 Glu Leu Ala Trp Ala Pro Asp Glu Ile Arg Glu Glu Val Asp Asn Asn
 595 600 605
 Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Asp Gln Gly Val
 610 615 620
 Gly Cys Ser Lys Val Pro Asp Ile His Asp Val Ala Leu Met Glu Asp
 625 630 635 640
 Arg Ala Thr Leu Arg Ile Ser Ser Gln Leu Leu Ala Asn Trp Leu Arg
 645 650 655
 His Gly Val Ile Thr Ser Ala Asp Val Arg Ala Ser Leu Glu Arg Met
 660 665 670
 Ala Pro Leu Val Asp Arg Gln Asn Ala Gly Asp Val Ala Tyr Arg Pro
 675 680 685
 Met Ala Pro Asn Phe Asp Asp Ser Ile Ala Phe Leu Ala Ala Gln Glu
 690 695 700
 Leu Ile Leu Ser Gly Ala Gln Gln Pro Asn Gly Tyr Thr Glu Pro Ile
 705 710 715 720
 Leu His Arg Arg Arg Arg Glu Phe Lys Ala Arg Ala Ala Glu Lys Pro
 725 730 735
 Ala Pro Ser Asp Arg Ala Gly Asp Asp Ala Ala Arg Val Gln Lys Tyr
 740 745 750
 Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg Val Ala Glu
 755 760 765

Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val Val Val Val
 770 775 780
 Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu Ala Gln Gln
 785 790 795 800
 Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu Leu Thr Ala
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 835 840 845
 Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr Pro Gly Arg
 850 855 860
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 865 870 875 880
 Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu Gly Arg Gly
 885 890 895
 Gly Ser Asp Thr Thr Ala Val Ala Met Ala Ala Ala Leu Gly Ala Asp
 900 905 910
 Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe Ser Ala Asp Pro
 915 920 925
 Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val Thr Phe Glu Glu
 930 935 940
 Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu Met Leu Arg Cys
 945 950 955 960
 Val Glu Tyr Ala Arg Arg His Asn Ile Pro Val His Val Arg Ser Ser
 965 970 975
 Tyr Ser Asp Arg Pro Gly Thr Val Val Val Gly Ser Ile Lys Asp Val
 980 985 990
 Pro Met Glu Asp Pro Ile Leu Thr Gly Val Ala His Asp Arg Ser Glu
 995 1000 1005
 Ala Lys Val Thr Ile Val Gly Leu Pro Asp Ile Pro Gly Tyr Ala Ala
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 Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln His Arg His Gly
 1025 1030 1035 1040
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Ile Gly Lys Val Ser Leu Ile Gly Ala Gly Met Arg Ser His Pro Gly
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 Glu Leu Ile Ser Thr Ser Glu Asp Gln Arg Ser Arg Cys Cys Ala Ala
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 Thr Pro Asn Trp Thr Arg Pro Trp Ser Arg Cys Met Lys Arg Ser Gly
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<210> 53

<211> 2952

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF15 fusion protein

<400> 53

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catcagggac aagggggcgc caagtccaag ggttctcagc aggaagacga ggcgctctac 2880
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<210> 54

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF15 fusion protein

<400> 54

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Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35 40 45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
50 55 60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Cys Gly Ser Lys Pro Pro
65 70 75 80
Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr
85 90 95
Pro Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu
100 105 110
Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro
115 120 125
Asn Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala
130 135 140
Gln Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu
145 150 155 160

Ser Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu
 165 170 175
 Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu
 180 185 190
 His Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr
 195 200 205
 Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val
 210 215 220
 Asn Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser
 225 230 235 240
 Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu
 245 250 255
 Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala
 260 265 270
 Val Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly
 275 280 285
 Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu
 290 295 300
 Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser
 305 310 315 320
 Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala
 325 330 335
 Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile
 340 345 350
 Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala
 355 360 365
 Ile Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln
 370 375 380
 Ala Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu
 385 390 395 400
 Asp Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser
 405 410 415
 Asp Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala
 420 425 430
 Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp
 435 440 445
 Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln
 450 455 460
 Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val
 465 470 475 480

Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile
 485 490 495
 Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
 500 505 510
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Thr Gln Ser Gln
 515 520 525
 Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn Arg Ala Asn Glu Val
 530 535 540
 Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val Pro Ile Thr Pro Cys
 545 550 555 560
 Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln Leu Val Leu Ser Ala
 565 570 575
 Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala Lys Glu Arg Gln Arg
 580 585 590
 Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala Tyr Gly Glu Val Asp
 595 600 605
 Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly Glu Gly Thr Val Gln
 610 615 620
 Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser Ser Ala Glu Leu Thr
 625 630 635 640
 Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro Asn Phe Met Asp Leu
 645 650 655
 Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp Gln Gly Ala Ser Leu
 660 665 670
 Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn Leu Thr Leu Gln Gly
 675 680 685
 Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp Glu Gly Asp Ala Ala
 690 695 700
 Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg Gln Trp Ile Leu His
 705 710 715 720
 Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln Ala Gln Tyr Val Ala
 725 730 735
 Gln Leu His Val Trp Ala Arg Arg Glu His Pro Thr Tyr Glu Asp Ile
 740 745 750
 Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro Ser Ala Arg Asp Gln
 755 760 765
 Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg Ser Glu Lys Val Leu
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 Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro Val Asn Pro Pro Lys
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<400> 57

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Thr Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu	
20 25 30	
aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct	144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser	
35 40 45	
cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg	192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu	
50 55 60	
acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg	240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala	
65 70 75	
gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg	288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala	
80 85 90 95	
agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt	336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly	
100 105 110	
ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg	384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg	
115 120 125	
cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
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cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
180 185 190	
act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
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Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
210 215 220	
gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	

tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser	768
240 245 250 255	
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu	816
260 265 270	
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala	864
275 280 285	
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu	912
290 295 300	
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala	960
305 310 315	
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu	1008
320 325 330 335	
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala	1056
340 345 350	
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370 375 380	
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400 405 410 415	
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln	1296
420 425 430	
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys	1344
435 440 445	
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala	1392
450 455 460	
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr	1440
465 470 475	

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ggt ccg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala 530 535 540	1632
gcg gcc aac cag gca gtc acc ccg gcg gcg ccg gcg ctg ccg ctg acc Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr 545 550 555	1680
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly 560 565 570 575	1728
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly 580 585 590	1776
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala 595 600 605	1824
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gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln 625 630 635	1920
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu 640 645 650 655	1968
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala 660 665 670	2016
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu 675 680 685	2064
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala 690 695 700	2112
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly 705 710 715	2160

ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc 2208
 Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val
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gtc ggg cac gcc cta taa gatatc
 Val Gly His Ala Leu 2232
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<210> 58

<211> 740

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: fusion protein
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<400> 58

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 35 40 45
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 85 90 95
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 100 105 110
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 115 120 125
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 130 135 140
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 145 150 155 160
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 165 170 175
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 180 185 190
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 195 200 205
 Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
 210 215 220
 Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
 225 230 235 240

Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
 245 250 255
 Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
 260 265 270
 Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
 275 280 285
 Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
 290 295 300
 Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr
 305 310 315 320
 Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
 325 330 335
 Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
 340 345 350
 Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
 355 360 365
 Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
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 Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
 385 390 395 400
 Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
 405 410 415
 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
 420 425 430
 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
 435 440 445
 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
 450 455 460
 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
 465 470 475 480
 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
 485 490 495
 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
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 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
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 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
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 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
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ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu	144
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65 70 75	
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile	288
80 85 90 95	
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100 105 110	
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr	384
115 120 125	
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro	432
130 135 140	
ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt atg Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met	480
145 150 155	
gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr	528
160 165 170 175	
gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp	576
180 185 190	
agc gtg gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val	624
195 200 205	
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240 245 250 255	
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260 265 270	

aac cgt gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa 864
 Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln
 275 280 285

aac acc ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg 912
 Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp
 290 295 300

gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg 960
 Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr
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gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc 1008
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 320 325 330 335

gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac 1056
 Ala Gly Gly Leu Leu Glu Gln Ala Ala Val Glu Glu Ala Ser Asp
 340 345 350

acc gcc gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa 1104
 Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln
 355 360 365

cag ctg gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt 1152
 Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly
 370 375 380

ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg 1200
 Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met
 385 390 395

gtg tcg atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg tcg 1248
 Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser
 400 405 410 415

atg acc aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg 1296
 Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala
 420 425 430

gcc gcc cag gcc gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg 1344
 Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met
 435 440 445

agc tcg ctg ggc agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg 1392
 Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val
 450 455 460

gcc gcc aac ttg ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg 1440
 Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro
 465 470 475

cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg 1488
 Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala
 480 485 490 495

ctg ccg ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag 1536
 Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln
 500 505 510

atg ctg ggc ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly	1584
515 520 525	
ggg ctc agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro	1632
530 535 540	
cat tct ccg gca gcc ggc aag ctt act caa ctc ctc aaa ttg ctt gcc His Ser Pro Ala Ala Gly Lys Leu Thr Gln Leu Leu Lys Leu Leu Ala	1680
545 550 555	
aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp	1728
560 565 570 575	
gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile	1776
580 585 590	
aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly	1824
595 600 605	
tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe	1872
610 615 620	
ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc ggc ttg tcg caa Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln	1920
625 630 635	
gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu	1968
640 645 650 655	
gct cac gcg gat agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala	2016
660 665 670	
ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag Gly Ile Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln	2064
675 680 685	
gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc cga gct gat ggc Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly	2112
690 695 700	
ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val	2160
705 710 715	
tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly	2208
720 725 730 735	
atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr	2256
740 745 750	

tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc 2304
 Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val
 755 760 765
 gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc 2352
 Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
 770 775 780
 taa cggcgaattc 2365

 <210> 60
 <211> 783
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: fusion protein
 HTCC#1(1-149)-TbH9-HTCC#1(161-392)

 <400> 60
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 1 5 10 15
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
 130 135 140
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met Val
 145 150 155 160
 Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala
 165 170 175
 Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser
 180 185 190
 Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val
 195 200 205
 Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met
 210 215 220

Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly
 225 230 235 240
 Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr
 245 250 255
 Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn
 260 265 270
 Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn
 275 280 285
 Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala
 290 295 300
 Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala
 305 310 315 320
 Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala
 325 330 335
 Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr
 340 345 350
 Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln
 355 360 365
 Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly
 370 375 380
 Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val
 385 390 395 400
 Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met
 405 410 415
 Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
 420 425 430
 Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser
 435 440 445
 Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala
 450 455 460
 Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln
 465 470 475 480
 Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu
 485 490 495
 Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met
 500 505 510
 Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly
 515 520 525
 Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His
 530 535 540

Ser Pro Ala Ala Gly Lys Leu Thr Gln Leu Leu Lys Leu Leu Ala Lys
 545 550 555 560
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
 565 570 575
 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
 580 585 590
 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
 595 600 605
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe
 610 615 620
 Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val
 625 630 635 640
 Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala
 645 650 655
 His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly
 660 665 670
 Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val
 675 680 685
 His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro
 690 695 700
 Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser
 705 710 715 720
 Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met
 725 730 735
 His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser
 740 745 750
 Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu
 755 760 765
 Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
 770 775 780

<210> 61

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
 HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<220>

<221> CDS

<222> (4)..(2439)

<400> 61

cat atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc	48
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly	
1 5 10 15	
atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg	96
Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu	
20 25 30	
aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct	144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser	
35 40 45	
cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg	192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu	
50 55 60	
acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg	240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala	
65 70 75	
gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg	288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala	
80 85 90 95	
agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt	336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly	
100 105 110	
ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg	384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg	
115 120 125	
cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
130 135 140	
cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
180 185 190	
act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg	672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
210 215 220	
gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	

tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser 240 245 250 255	768
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu 260 265 270	816
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala 275 280 285	864
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu 290 295 300	912
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala 305 310 315	960
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu 320 325 330 335	1008
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala 340 345 350	1056
atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala 355 360 365	1104
gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr 370 375 380	1152
ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu 385 390 395	1200
ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala 400 405 410 415	1248
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln 420 425 430	1296
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys 435 440 445	1344
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala 450 455 460	1392
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr 465 470 475	1440

ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala 480 485 490 495	1488
gtg caa acc gcg gcg caa aac ggg gtc ccg gcg atg agc tcg ctg ggc Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly 500 505 510	1536
agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu 515 520 525	1584
ggc ccg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala 530 535 540	1632
gcg gcc aac cag gca gtc acc ccg gcg gcg ccg gcg ctg ccg ctg acc Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr 545 550 555	1680
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly 560 565 570 575	1728
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly 580 585 590	1776
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala 595 600 605	1824
gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser 610 615 620	1872
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln 625 630 635	1920
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu 640 645 650 655	1968
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala 660 665 670	2016
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu 675 680 685	2064
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala 690 695 700	2112
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly 705 710 715	2160

ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc 2208
 Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val 720 725 730 735
 gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc 2256
 Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly 740 745 750
 gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg 2304
 Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr 755 760 765
 ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag 2352
 Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu 770 775 780
 ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc 2400
 Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile 785 790 795
 atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc taa gatatc 2445
 Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile 800 805 810

<210> 62
 <211> 811
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: fusion protein
 HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<400> 62
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 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 20 25 30
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 35 40 45
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 85 90 95
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 100 105 110
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 115 120 125
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 130 135 140

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
145 150 155 160
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
165 170 175
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
180 185 190
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
195 200 205
Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
210 215 220
Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
225 230 235 240
Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
245 250 255
Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
260 265 270
Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
275 280 285
Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
290 295 300
Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr
305 310 315 320
Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
325 330 335
Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
340 345 350
Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
355 360 365
Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
370 375 380
Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
385 390 395 400
Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
405 410 415
Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
420 425 430
Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
435 440 445
Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
450 455 460

Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
 465 470 475 480
 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
 485 490 495
 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
 500 505 510
 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
 515 520 525
 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
 530 535 540
 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
 545 550 555 560
 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
 565 570 575
 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
 580 585 590
 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
 595 600 605
 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
 610 615 620
 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
 625 630 635 640
 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
 645 650 655
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
 660 665 670
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
 675 680 685
 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
 690 695 700
 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
 705 710 715 720
 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
 725 730 735
 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
 740 745 750
 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
 755 760 765
 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
 770 775 780

Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
 785 790 795 800

Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
 805 810

<210> 63
 <211> 1629
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 TbRa12-HTCC#1

<220>
 <221> CDS
 <222> (4)..(1623)

<400> 63
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 Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln
 1 5 10 15
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 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
 20 25 30
 gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His
 35 40 45
 atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
 Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
 50 55 60
 aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
 Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
 65 70 75
 ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
 Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
 80 85 90 95
 atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
 Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
 100 105 110
 ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
 Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
 115 120 125
 aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc cta gta 432
 Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val
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gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln 160 165 170 175	528
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 465 470 475

tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct 1488
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 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
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 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
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 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
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 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val Pro
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 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
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 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
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 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
 195 200 205
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
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 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
 245 250 255
 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
 260 265 270
 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
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 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
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 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
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 Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
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 Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn
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 Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu
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<210> 95
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<220>
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<400> 95
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<210> 96
 <211> 60
 <212> DNA
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<220>
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 sequence of HTCC#1 peptide 3 for T-cell epitope
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<400> 96
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<210> 97
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 4 for T-cell epitope
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<400> 97
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<210> 98
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 <212> DNA
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<220>
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<400> 98
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<210> 99
 <211> 60
 <212> DNA
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 <220>
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 sequence of HTCC#1 peptide 6 for T-cell epitope
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 <210> 100
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 <210> 101
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 8 for T-cell epitope
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 <400> 101
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 <210> 102
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 9 for T-cell epitope
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 <400> 102
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 <210> 103
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 10 for T-cell epitope
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<400> 103
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<210> 104
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 11 for T-cell epitope
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<400> 104
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<210> 105
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 <212> DNA
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<220>
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<400> 105
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<210> 106
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<220>
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<400> 106
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<210> 107
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 sequence of HTCC#1 peptide 14 for T-cell epitope
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<210> 108
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<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 15 for T-cell epitope
 mapping

<400> 108
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<210> 109
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<220>
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 sequence of HTCC#1 peptide 16 for T-cell epitope
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<400> 109
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<210> 110
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<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 17 for T-cell epitope
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<210> 111
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<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 18 for T-cell epitope
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<400> 111
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<210> 112
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 <210> 113
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 <210> 114
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 <210> 115
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 22 for T-cell epitope
 mapping

 <400> 115
 gccagcttgc ccgccctggc cggcattggg ggcgggtccg gttttggggg cttgccgagc 60

 <210> 116
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 23 for T-cell epitope
 mapping

<400> 116
 ggttttgggg gcttgccgag cctggctcag gtccatgccg cctcaactcg gcaggcgcta 60

<210> 117
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 24 for T-cell epitope
 mapping

<400> 117
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<210> 118
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 25 for T-cell epitope
 mapping

<400> 118
 ccggtcggcg ccgctgccga gcaggtcggc gggcagtcgc agctggtctc cgcgcagggt 60

<210> 119
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 26 for T-cell epitope
 mapping

<400> 119
 cagctggtct ccgcgcaggg ttcccaaggt atgggcggac ccgtaggcac gggcggc 57

<210> 120
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 27 for T-cell epitope
 mapping

<400> 120
 cccgtaggca tgggcggcat gcacccctct tcgggggcgt cgaaaggac gacgacgaag 60

<210> 121
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 28 for T-cell epitope
 mapping

<400> 121
 tcgaaaggga cgacgacgaa gaagtactcg gaaggcgcgg cggcgggcac tgaagacgcc 60

<210> 122
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 29 for T-cell epitope
 mapping

<400> 122
 gcggcgggca ctgaagacgc cgagcgcgcg ccagtcgaag ctgacgcggg cggtgggcaa 60

<210> 123
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nucleic acid
 sequence of HTCC#1 peptide 30 for T-cell epitope
 mapping

<400> 123
 cgcgcgccag tcgaagctga cgcgggcggg gggcaaaagg tgctggtacg aaacgtcgtc 60

<210> 124
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 1 for T-cell epitope mapping

<400> 124
 Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Leu
 20

<210> 125
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
2 for T-cell epitope mapping

<400> 125
Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
1 5 10 15
Gly Ile Leu Tyr
20

<210> 126
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
3 for T-cell epitope mapping

<400> 126
Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala
1 5 10 15
Leu Glu Glu Leu
20

<210> 127
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
4 for T-cell epitope mapping

<400> 127
Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp
1 5 10 15
Leu Gly Ser Ala
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<210> 128
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
5 for T-cell epitope mapping

<400> 128
 Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg
 1 5 10 15
 Asn His Val Asn
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<210> 129
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 6 for T-cell epitope mapping

<400> 129
 Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu Asp
 1 5 10 15
 Arg Gln Leu Ile
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<210> 130
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 7 for T-cell epitope mapping

<400> 130
 Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala
 1 5 10 15
 Val Gln Thr Thr
 20

<210> 131
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 8 for T-cell epitope mapping

<400> 131
 Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys
 1 5 10 15
 Gly Leu Glu Phe
 20

<210> 132
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
9 for T-cell epitope mapping

<400> 132
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
1 5 10 15
Tyr Ile Pro Val
20

<210> 133
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
10 for T-cell epitope mapping

<400> 133
Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe
1 5 10 15
Gln Ala Pro Phe
20

<210> 134
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
11 for T-cell epitope mapping

<400> 134
Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly
1 5 10 15
Gly Ala Leu Ala
20

<210> 135
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
12 for T-cell epitope mapping

<400> 135

Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn
1 5 10 15

Ala Thr Gln Leu
20

<210> 136

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
13 for T-cell epitope mapping

<400> 136

Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu
1 5 10 15

Leu Val Ala Ala
20

<210> 137

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
14 for T-cell epitope mapping

<400> 137

Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
1 5 10 15

Ala Asp Ile Ile
20

<210> 138

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
15 for T-cell epitope mapping

<400> 138

Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu
1 5 10 15

Phe Ile Thr Asn
20

<210> 139
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
16 for T-cell epitope mapping

<400> 139
Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp
1 5 10 15
Asp Lys Leu Thr
20

<210> 140
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
17 for T-cell epitope mapping

<400> 140
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
1 5 10 15
Gly Trp Ser Asn
20

<210> 141
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
18 for T-cell epitope mapping

<400> 141
Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
1 5 10 15
Gly Leu Thr Gly
20

<210> 142
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
19 for T-cell epitope mapping

<400> 142

Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr
1 5 10 15

Gly Leu Phe Gly
20

<210> 143

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
20 for T-cell epitope mapping

<400> 143

Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly
1 5 10 15

Leu Ala His Ala
20

<210> 144

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
21 for T-cell epitope mapping

<400> 144

Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
1 5 10 15

Pro Ala Leu Ala
20

<210> 145

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
22 for T-cell epitope mapping

<400> 145

Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly
1 5 10 15

Gly Leu Pro Ser
20

<210> 146
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
23 for T-cell epitope mapping

<400> 146
Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr
1 5 10 15
Arg Gln Ala Leu
20

<210> 147
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
24 for T-cell epitope mapping

<400> 147
Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly
1 5 10 15
Ala Ala Ala Glu
20

<210> 148
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
25 for T-cell epitope mapping

<400> 148
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
1 5 10 15
Ser Ala Gln Gly
20

<210> 149
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
26 for T-cell epitope mapping

<400> 149

Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
1 5 10 15

Met Gly Gly

<210> 150

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
27 for T-cell epitope mapping

<400> 150

Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly
1 5 10 15

Thr Thr Thr Lys
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<210> 151

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
28 for T-cell epitope mapping

<400> 151

Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly
1 5 10 15

Thr Glu Asp Ala
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<210> 152

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
29 for T-cell epitope mapping

<400> 152

Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala
1 5 10 15

Gly Gly Gly Gln
20

<210> 153
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 30 for T-cell epitope mapping

<400> 153
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
 1 5 10 15
 Arg Asn Val Val
 20

<210> 154
 <211> 84
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> secreted form of DPPD

<400> 154
 Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro
 1 5 10 15
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 20 25 30
 Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr
 35 40 45
 Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro
 50 55 60
 Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln
 65 70 75 80
 Pro Asn Ala Pro

<210> 155
 <211> 2836
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI-A)

<400> 155
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 gcccggcggt gtcggcgagt ttggcgcggg cggagccggt cgggagggtg tcggtgccgc 360
 caagttgggc cgtcgcggt ccggccttcg cggagaagcc tgaggcgggc acgccgatgt 420
 ccgtcatcgg cgaagcgtcc agctgcggtc agggaggcct gcttcgaggc ataccgctgg 480


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<210> 156
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: MtB9.9A (MTI-A)
      ORF peptide

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<400> 156
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
  1               5               10              15

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<210> 157
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 157
 Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 1 5 10 15

<210> 158
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 158
 Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
 1 5 10 15

<210> 159
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 159
 Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
 1 5 10 15

<210> 160
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 160
 Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
 1 5 10 15

<210> 161
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 161
 Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
 1 5 10 15

<210> 162
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 162
 Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
 1 5 10 15

<210> 163
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 163
 Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
 1 5 10 15

<210> 164
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 164
 Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
 1 5 10 15

<210> 165
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MtB9.9A (MTI-A)
 ORF peptide

<400> 165
 Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
 1 5 10 15

<210> 166
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 166

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15

Gln Ala

<210> 167
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 167

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 168

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

<210> 169
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 169

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

<210> 170
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 170
Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

<210> 171
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 171
Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

<210> 172
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 172
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
1 5 10 15

<210> 173
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 173
Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

<210> 174
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 174
 Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1 5 10 15

<210> 175
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 175
 Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
 1 5 10 15

<210> 176
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 176
 Lys Ala Gly Leu Met His Thr Ile Gly Gln Ala Glu Gln Ala
 1 5 10

<210> 177
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 177
 Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
 1 5 10 15

<210> 178
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 178

Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
1 5 10 15

<210> 179

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 179

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

<210> 180

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 180

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

<210> 181

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 181

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

<210> 182

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 182

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val
1 5 10 15

<210> 183
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 183
Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 184
Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

<210> 185
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 185
Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

<210> 186
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 186
Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15

Asp Ala

r

<210> 187
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-294

 <400> 187
 cgtaatcacg tgcagaagta cggcggatc

29

<210> 188
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-295

 <400> 188
 ccgactagaa ttcactattg acaggcccat c

31

<210> 189
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-268

 <400> 189
 ctaagtagta ctgatcgcgt gtcggtgggc

30

<210> 190
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-296

 <400> 190
 catcgatagg cctggccgca tcgtcacc

28

<210> 191
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-157

<400> 191
 ctagttagta ctcagtcgca gaccgtg 27

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-160

<400> 192
 gcagtgcga attcacttcg actcc 25

<210> 193
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-69

<400> 193
 ggatccagcg ctgagatgaa gaccgatgcc gct 33

<210> 194
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-83

<400> 194
 ggatatctgc agaattcagg tttaaagccc atttgcga 38

<210> 195
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-192

<400> 195
 tgtggctcga aaccaccgag cggttc 26

<210> 196
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-60

 <400> 196
 gagagaattc tcagaagccc atttgcgagg aca 33

 <210> 197
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 oligonucleotide 5' primer

 <400> 197
 caattacata tgcatacaca tcaccatcac atgagcagag cgttcacat c 51

 <210> 198
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 oligonucleotide 3' primer

 <400> 198
 catggaattc gccgttagac gacgtttcgt a 31

 <210> 199
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide 5' primer

 <400> 199
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 <210> 200
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide 3' primer

 <400> 200
 ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 201
 <211> 1179
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
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 <222> (1)..(1179)
 <223> HTCC#1

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<400> 201
atg agc aga gcg ttc atc atc gat cca acg atc agt gcc att gac ggc      48
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1             5             10             15

ttg tac gac ctt ctg ggg att gga ata ccc aac caa ggg ggt atc ctt      96
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
             20             25             30

tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag gag ctg gca gca     144
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
             35             40             45

gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg gac aaa tac gcc     192
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
             50             55             60

ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa ctg gca gac ctc     240
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
             65             70             75             80

gat cgt cag ctc atc agc ctg atc cac gac cag gcc aac gcg gtc cag     288
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
             85             90             95

acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt ctc gag ttc gtg     336
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
             100             105             110

cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc gtc ggg cac gcc     384
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
             115             120             125

cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc gcg atg gcc gta     432
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
             130             135             140

gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg ctg atc aac gcg     480
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
             145             150             155             160

act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc     528
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
             165             170             175

gcc att gcg gac atc att tcg gat gtg gcg gac atc atc aag ggc atc     576
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
             180             185             190

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ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa 624
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205

gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga 672
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220

ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc 720
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240

ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc 768
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255

ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc 816
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270

tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt 864
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285

ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag 912
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300

gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag 960
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg 1008
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg 1056
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act 1104
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 1152
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380

aag gtg ctg gta cga aac gtc gtc taa 1179
 Lys Val Leu Val Arg Asn Val Val
 385 390

<210> 202

<211> 392

<212> PRT

<213> Mycobacterium tuberculosis

<400> 202

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380

Lys Val Leu Val Arg Asn Val Val
385 390